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GGCGCGGCCGCCCCGAGGCAGGAGCAAGAGGCAGCCGGAGCCGAGGATCCAC
GCCGCCGCGCGCCATGGAGCCCAGTGAGCGCGCGCTCCGGCCGCCGCCGCT
GACGACATGGAAACGGCGCCGACCCGGCCCTCCGCCGCCGCCGCCGCT
GCTGCTGCTGGTGCTGTACTGCAGCTTGGTCCCCGCCGGCCTCACCGCTCC
TGTTGTTGCCAACCGCCGGATGTGCGGCTAGTGGATGCCGGCGGAGTGAAG
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CCCGTAAGGTTCTCTTCTGGCAGGACCTGGACCAGCCAAGGCCATTGCCCTG
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CGAGCGGGCAGGGATGGATGGCAGTACCCGGAAGATCATTGTAGACTCCGACA
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GCCGATGCCAAGCTCAGCTTCATCCACCGTGCCAACCTGGACGGCTCTTCCG
GCAGAAGGTGGTGGAGGGCAGCCTCACTCACCCCTTGCCCTGACACTCTCTG
GGGACACACTCTACTGGACAGACTGGCAGACCCGCTCATCCACGCCGCAAC
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TTCTACTCCTGTGCCCTGCCCCACTGGTGTGCAGTTGCAGGACAATGGCAAGAC
GTGCAAGACAGGGCTGAGGAAGTGCTGCTGGCTCGGAGGACAGACCTGA
GGAGGATCTCTGGACACCCCTGACTCACAGACATAGTGCTGCAGGTGGC
GACATCCGGCATGCCATTGCCATTGACTACGATCCCTGGAGGGTACGTGTA
CTGGACCGATGATGAGGTGCGGGCTATCCGCAGGGCGTACCTAGATGGCTCAG
GTGCCAGACACTTGTGAACACTGAGATCAATGACCCGATGGCATTGCTGTG
GACTGGTCGCCCGGAACCTCTACTGGACAGATAACAGGCACTGACAGAAATTGA
GGTGAECTGCCCTAACGGCACCTCCGAAAGATCCTGGTATCTGAGGACCTGG
ACGAACCGCAGGCCATTGTGTTGCACCCGTGATGGGCTCATGTACTGGACA
GACTGGGGGAGAACCCAAAATCGAATGCCAACCTAGATGGAGAGAGATCG
GCATGTCCCTGGTAACACCTCCCTGGTGGCCAATGGACTGCCCTGGACC
TGCAGGAGGGCAAGCTGACTGGGGGATGCCAAAATGATAAAATCGAGGTG
ATCAACATAGACGGACAAAGCGGAAGACCCGTGCTTGAGGACAAGCTCCACA
CATTTTGTTGGTTCACACTGCTGGGGACTTCATCTACTGGACCGACTGGCAGA
GACGCAGTATTGAAAGGGTCCACAAGGTCAAGGCCAGCCGGATGTCATCATT
GATCAACTCCCCGACCTGATGGGACTCAAAGCCGTGAATGTGCCAAGGTTGT
CGGAACCAACCCATGTGCGGATGGAAATGGAGGGTGCAGCCATCTGCTTCT
TCACCCCCACGTGCCACCAAGTGTGGCTGCCCTGGCCTGGAGCTGTTGAGT
GACATGAAGACCTGCATAATCCCCGAGGCCTTCCCTGGTATTCAACCAGCAGAGC
CACCATCCACAGGATCTCCCTGGAGACTAACAAACAACGATGTGGCTATCCCAC
TCACGGGTGTCAAAGAGGGCCTGCACTGGACTTGTGTCACAAACAATCAG

FIGURE 1A

ATCTACTGGACTGATGTTAGCCTCAAGACGATCAGCCAGCCTTCATGAATGG
GAGCTCAGTGGAGCACGTGATGAGTTGGCCTCGACTACCCTGAAGGAATGG
CTGTGGACTGGATGGCAAGAACCTCTATTGGCGGACACAGGGACCAACAGG
ATTGAGGTGGCCCGGCTGGATGGCAGTTCCGGCAGGTGCTTGTGGAGAGA
CCTTGACAACCCCAGGTCTGGCTCTGGATCCTACTAAAGGCTACATCTACT
GGACTGAGTGGGTGGCAAGCCAAGGATTGTGCGGGCCTCATGGATGGGACC
AATTGTATGACACTGGTAGACAAGGTGGCCGGCAACGACCTCACCATTA
TTATGCCGACCAGCGACTGTACTGGACTGACCTGGACACCAACATGATTGAGT
CTTCCAACATGCTGGTCAGGAGCGCATGGTGTAGCTGACGATCTGCCCTAC
CCGTTGGCCTGACTCAATATAGCGATTACATCTACTGGACTGACTGGAACCT
GCATAGCATTGAACGGGCGGACAAGACCAGTGGCGGAACCGCACCCCTCATCC
AGGGTCACCTGGACTTCGTATGGACATCCTGGTGTCCACTCCTCCGTCAG
GATGGCCTCAACGACTGCGTGCACAGCAATGCCAGTGTGGCAGCTGTGCCT
CGCCATCCCCGGAGGCCACCGCTGTGGCTGTGCTCACACTACACGCTGGACC
CCAGCAGCCGCACTGCAGCCGCCCTCCACCTTCTGCTGTTAGCCAGAAA
TTTGCCATCAGCCGGATGATCCCCGATGACCAAGCTCAGCCGGACCTTGTCC
ACCCCTCATGGCTGAGGAACGTCAAAGCCATCAACTATGACCCGCTGGACA
AGTTCATCTACTGGTGGACGGCGCCAGAACATCAAGAGGGCCAAGGACGAC
GGTACCCAGCCCTCCATGCTGACCTCTCCAGCCAAGCCTGAGCCAGACAG
ACAGCCACACGACCTCAGCATTGACATCTACAGCCGGACACTGTTCTGGACCT
GTGAGGCCACCAACACTATCAATGTCCACCGGCTGGATGGGATGCCATGGGA
GTGGTCTCGAGGGGACCGTGACAAGCCAAGGGCATTGCTGTCAATGCTGA
GCGAGGGTACATGTACTTTACCAACATGCAGGACCATGCTGCCAAGATCGAGC
GAGCCTCCCTGGATGGCACAGAGCGGGAGGTCTTCAACCACAGGCCTCATC
CGTCCCCTGGCCCTTGTGGACAATGCTCTGGCAAGCTCTGGTGG
TGCCGACCTAAAGCGAATCGAAAGCTGTGACCTCTGGGCAACCGCCTGA
CCCTGGAAAGATGCCAACATCGTACAGCCAGTAGGTCTGACAGTGCTGGCAGG
CACCTCTACTGGATCGACCGCCAGCAGCAGATGATCGAGCGCGTGGAGAAGAC
CACTGGGGACAAGCGGACTAGGGTTAGGGCCGTGTCACCCACCTGACAGGCA
TCCATGCCGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCTGTGCC
CGAGACAATGGCGGCTGCTCCACATCTGTATGCCAAGGGTGTGGAAACACC
GCGCTGCTCGTGCCTGTCCACCTGGTGTCTGCAGAACCTGCTGACTTGTG
GTGAGCCTCCTACCTGCTCCCTGATCAGTTGCATGTACCACTGGTGGAGATC
GACTGCATCCCCGGAGCCTGGCGCTGTGACGGCTCCCTGAGTGTGCTGACCA
GAGTGATGAAGAAGGCTGCCAGTGTGCTCCGCTCTCAGTTCCCTGCGCTC
GAGGCCAGTGTGTGGACCTGCGGTTACGCTGCGACGGTGAGGCCAGTGCCAG
GATCGCTCTGATGAAGCTAACTGCGATGCTGTCTGCTGCCAATCAGTTCCG
GTGCACCAGCGGCCAGTGTGCTCATCAAGCAACAGTGTGACTCCTCCCG
ACTGTGCTGATGGGTCTGATGAGCTCATGTGTGAAATCAACAAGCCACCCCT
GATGACATCCCAGCCCCACAGCAGTGCCATTGGGCCGTGATTGGTATCATCCT
CTCCCTCTCGTATGGCGGGGTCTACTTGTCTGCCAGCGTGTGATGTGCC

FIGURE 1B

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AGCGCTACACAGGGGCCAGTGGGCCCTTCCCCACGAGTATGTTGGTGGAGCC
CCTCATGTGCCTCTCAACTTCATAGCCCCAGGTGGCTCACAGCACGGTCCCTT
CCCAGGCATCCCGTGCAGCAAGTCCGTGATGAGCTCCATGAGCCTGGTGGGGG
GGCGCGGCAGCGTGCCCCCTATGACCGGAATCACGTCACTGGGCCTCATCC
AGCAGCTCGTCCAGCACAAAGGCCACACTATATCCGCCGATCCTGAACCCACC
CCC GTCCCCGGCCACAGACCCCTCTCTACAACGTGGACGTGTTATTCTT
CAGGCATCCCGGCCACCGCTAGACCATA CAGGCCCTACGTCAATTGAGGTATG
GCACCCCCAACAACACCGTGCAGCACAGATGTGTGACAGTGA C TACAGCAT
CAGTCGCTGGAAGAGCAGCAAATACTACCTGGACTTGAATTGGACTCAGACC
CCTACCCCCCCCCGCCACCCCCCACAGCCAGTACCTATCTGCAGAGGACAGC
TGCCCACCCCTCACCAGGC ACTGAGAGGAGTTACTGCCACCTCTCCGCC
ACCGTCCCCCTGCACGGACTCGTCCTGACCTCGGCCGTCCACCCGGCCCTGCT
GCCTCCCTGTAAATATTTTAAATATGAACAAAGGAAAAATATATTTATGAT
TTAAAAAATAAATATAATTGGGTTTAACAAGTGAGAAATGTGAGCGGTGA
AGGGGTGGGCAGGGCTGGAAACTTTCTAG (SEQ ID NO: 7)

FIGURE 1C

49

METAPTRAPPPPPPLLLVLYCSLVPAASPLLLFANRRDVRLVDAGGVKLE
STIVASGLEAAAVDFQFSKGAVYWTDVSEEAIKQTYLNQTGAAAQNIVISGL
VSPDGLACDWVGKKLYWTDSETNRIEVANLNGTSRKVLFWQDLDQPRAIALDP
AHGYMYWTDWGEAPRIERAGMDGSTRKIIVDSDIYWPNGLTIDLEEQKLYWAD
AKLSFIHRANLDGSFRQKVVEGSLTHPFALTSGDTLYWTDWQTRSIHACNKW
TGEQRKEILSALYSPMIDIQLSQERQPFHTPCEEDNGGCSHLCLLSPREPFY
SCACPTGVQLQDNGKTCKTGAEVLLARRDLRRISLDTPDFTDIVLQVGDI
RHAIADYDPLEGYVYWTDDEVRAIRRAYLDGSGAQTLVNTEINDPDGIAVDW
VARNLWTDGTDRIEVTRLNGTSRKILVSEDLDEPRAIVLHPVMGLMYWTDW
GENPKIECANLDGRDRHVLVNTSLGPNGLALDLQEGKLYWGDAKTDKIEVIN
IDGTRKRTLLEDKLPHIFGFTLLGDFIYWTDWQRRSIERVHKVKASRDVIIDQ
LPDLMGLKAVNVAKVVGTNPCADGNNGCSHLCFFTPRATCGCPIGLELLSDM
KTCIIPEAFLVFTSRATIHRISLETNNNDVAIPLTVKEASALDFDVSNHHIY
WTDVSLKTISRASFNMGSVEHVIEFGLDYPEGMAVDWMGKNLYWADTGTNRIE
VARLDGQFRQVLVWRDLNDNPRSLALDPTKGYYIWTEWGGKPRIVRAFMMDGTNC
MTLVDKVGRANDLTIDYADQRLYWTDLDTNMIESSNMLQERMVIADDLPYPF
GLTQYSDYIYWTDWNLHSIERADKTSGRNRTLIQGHLDVMDILVFHSSRQDG
LNDCVHSNGQCGQLCLAIPGGHRCGCASHYTLDPSSRNCSPPSTFLFSQKFA
ISRMIPDDQLSPDVLPLHGLRNVKAINYDPLDKFIYWDGRQNIKRAKDDGT
QPSMLTSPSQLSPDRQPHDLSIDIYSRTLFWTCEATNTINVHRLDGDAMGVV
LRGDRDKPRAIAVNAERGYMYFTNMQDHAAKIERASLDGTEREVLFTTGLIRP
VALVVDNALGKLFWVDADLKRIESCDLSGANRLTLEDANIVQPVGLTVLGRHL
YWIDRQQQMIEERVEKTTGDKRTRVQGRVTHLTGIHAVEEVSLEEFSAHPCARD
NGGCSHICIAKGDTPRCSCPVLVLLQNLTCGEPPCTCSPDQFACTTGEIDC
IPGAWRCDGFPECADQSDEEGCPVCSASQFPCARGQCVDLRLRCDGEADCQDR
SDEANCAVCLPNQFRCTSGQCVLIKQQCDSFPDCADGSDELMCEINKPPSDD
IPAHSAAIGPVIGIILSLFVMGGVYFVCQRVMCQRYTGASGPFPHEYVGGAPH
VPLNFIAPGGSQHGPFPGPICSKSVMSMSLVGGGRGSVPLYDRNHVTGASSSS
SSSTKATLYPPILNPPPSPATDPSLYNVDVFYSSGIPATARPYRPYVIRGMAP
PTTPCSTDVCDSDYSISRWKS SKYYLDLNSDSDPYPPPPTPHSQYLSAEDSCP
PSPGTERSÝCHLFPPPSPCTDSS (SEQ ID NO: 2)

FIGURE 2

Construct

Gene: 193

GI Number(s): 6678715

Gene Family: EGF domain protein

Gene Subfamily: Low-density lipoprotein receptor

Gene Sequence: full-length cDNA, Mouse

underlined = deleted in targeting construct

[] = sequence flanking Neo insert in targeting construct

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GCCGCGCGCCCGAGGCAGGGAGCAAGAGGCAGGGAGCCCGAGGGATCCACCGCCGCC
CGCGCGCCATGGAGCCCCAGTGAGCGCGCCGCTCCCGCCGCCGACGACATGGAAAC
GGCGCCGACCCGGGCCCCCTCCGCCGCCGCCGCTGCTGCTGGTGTGTACTG
CAGCTTGGTCCCCGCCGCCCTCACCGCTCTGTTGCAACCCGGGGATGTGCG
GCTAGTGGATGCCGCCGGAGTCGAAGCTGGAGTCCACCATGGCCAGTGGCTTGGAGGA
TGCAGCTGCTGTAGACTTCCAGCTCCAAGGGTGCTGTACTGGACAGATGTGAGCGA
GGAGGCCATCAAACAGACCTACCTGAACCAAGACTGGAGCTGCTGACAGAACATTGTCA
CTCGGGCTCGTGTACCTGATGGCTGGCTGTGACTGGGTTGCAAGAACAGTGTACTG
GACGGACTCCGAGACCAACCGCATTGAGGTGCCAACCTCAATGGACGTCCCCTAAGGT
TCTCTTCTGGCAGGACCTGGACCAGCCAAGGGCATTGCCCTGGATCCTGCACATGGTA
CATGTACTGGACTGACTGGGGGAAGCACCCTGGATCGAGCGGGCAGGGATGGATGGCAG
TACCCGGAAGATCATTGTAGACTCCGACATTACTGGCCAATGGCTGACCACGACCT
GGAGGAACAGAACAGTGTACTGGGGCAGTCCAAGCTCAGCTTCACTCACCCTGCCAACCT
GGACGGCTCCTCCCGCAGAACGGTGGAGGGCAGCCTCACTCACCCTTGCCCTGAC
ACTCTCTGGGACACACTCTACTGGACAGACTGGCAGACCCGCTCCATCCACCCCTGCAA
CAAGTGGACAGGGGAGCAGAGGAAGGAGATCCTTAGTGCTCTGTACTCACCCATGGACAT
CCAAGTGTGAGCCAGGAGCGCAGCCTCCCTTCACACACCACGAGGGAGGACAACGG
TGGCTGTTCCCACCTGTGCCTGCTGTCCCCGAGGGAGCCTTCTACTCCTGTGCCTGCC
CACTGGTGTGCAGTTGCAAGGACAATGGCAAGACGTGCAAGACAGGGCTGAGGAAGTGT
GCTGCTGGCTGGAGGACAGACCTGAGGGAGATCTCTGGACACCCCTGACTTCACAGA
CATAGTGTGCTGAGGAGCTGGGAGCATGGCATTGCCATTGCACTACGATCCCTGGAA
GGGCTACGTGTACTGGACCGATGATGGGTGCGGGCTATCCGCAAGGGCTACCTAGATGG
CTCAGGTGCGCAGACACTTGGAACACTGAGATCAATGACCCCGATGGCATTGCTGTGGA
CTGGGTGCCCCGGAACCTCTACTGGACAGATACTGGCAAGGACTGACAGAAATTGAGGTGACTCG
CCTCAACGGCACCTCCGAAAGATCCTGGTATCTGAGGACCTGGACGAACCGCGAGCCAT
TGTGTTGACCCCTGTGATGGGCTCATGTACTGGACAGACTGGGGGAGAACCCAAAAT
CGAATGCGCAACCTAGATGGGAGAGATCGGCATGTCTGGTGAACACCTCCCTGGGTG
GCCCAATGGACTGGCCCTGGACCTGCGAGGGAGGCAAGCTGACTGGGGGGATGCCAAAAC
TGATAAAATCGAGGTGATCAACATAGACGGGACAAGGGGAACCCCTGCTTGAGGACAA
GCTCCACACATTTGGGTTCAACTGTGGGGGACTTCATCTACTGGACCGACTGGCA
GAGACCGAGTATTGAAAGGGTCCACAAGGTCAAGGCCAGCCGGGATGTCATCATTGATCA
ACTCCCCGACCTGATGGGACTCAAAGCCGTGAATGTGGCCAAGGGTGTGGAACCAACCC
ATGTGCGGATGGAAATGGAGGGTGCAGCCATCTGTGCTTCTTCACCCACGTGCCACCAA
GTGTGGCTGCCCTATTGGCTGGAGCTGTGAGTGACATGAAGACCTGCTGATAATCCCCGA
GGCCTTCTGGTATTCAACAGAGCCACCATCCACAGGATCTCCCTGGAGGACTAACAA
CAACGATGTGGCTATCCACTCACGGGTCTGCACTGGGACTTTGATGT
GTCCCAACATCACATCTACTGGACTGATGTTAGCTCAAGACGATCAGCCGAGCCTTCAT
GAATGGGAGCTAGTGGAGCACGTGATTGAGTTGGCTCGACTACCCCTGAGGAAATGGC
TGTGGACTGGGAGCTGATGGGAGGACACAGGGACCAACAGGGATTGAGGTT
GGCCCGGGCTGGATGGCAGTCCGGCAGGTGCTGTGAGGAGACCTTGACAACCCCAAG
GTCTCTGGCTCTGGATCCCTACTAAAGGCTACATCTACTGGACTGAGTGGGGTGGCAAGCC
AAGGATTGTGCGGGCTTCATGGATGGGACCAATTGTATGACACTGGTAGACAAGGTGGG
CCGGGCAACGACCTCACCATTGATTATGCCGACCCAGCGACTGTACTGGACTGACCTGGA
GACCAACATGATTGAGTCTTCACATGCTGGGTCAAGGAGGCGATGCTGATAGCTGACCA

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FIGURE 3A

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TCTGCCCTACCCGTTGGCCTGACTCAATAAGCGATTACATCTACTGGACTGACTGGAA
CCTGCATAGCATTGAACGGGGACAAGAACAGTGGCGGAACCGCACCCCATCCAGGG
TCACCTGGACTTCGTATGGACATCCTGGTGTCCACTCCTCCCGTCAGGATGGCCTCAA
CGACTGCGTGACAGCAATGGCAGTGTGGCAGCTGTGCGCATCCCCGGAGGCCA
CCGCTGTGGCTGTGCTTCACACTACACGCTGGACCCAGCAGCCCAACTGCAGCCC
CTCCACCTCTTGTGTTCAGCCAGAAATTGCCATAGCCGGATGATCCCCGATGACCA
GCTCAGCCCGGACCTTGTCTACCCCTCATGGGCTGAGGAACGTCAAAGCCATCAACTA
TGACCCGCTGGACAAGTTCATCTACTGGGTGGACGGCGCCAGAACATCAAGAGGGCCAA
GGACGACGGTACCCAGCCCTCATGCTGACCTCTCCAGCCAAAGCCTGAGGCCAGACAG
ACAGCCACACGACCTCAGCATGACATCTACAGCCGACACTGTTCTGGACCTGTGAGGC
CACCAACACTATCAATGTCCACGGCTGGATGGGATGCCATGGGAGTGGTGTGCTTGAGG
GGACCGTGACAAGGCCATTGCTGCAATGCTGAGCGAGCCCTGGATGGCACAGAGC
GGTCTCTTCACCACAGGCCTCATCCGTCCCCTGTTGTTGACAATGCTCTGGG
CAAGCTCTCTGGGTGGATGCCGACCTAACCGAATCGAAAGCTGTGACCTCTCTG [GGG
CCAACCCGCTGACCTGGAAGATGCCAACATCGTACAGCAGTAGGTCTGACAGTGCTGG
GCAGGCACCTACTGGATCGACCGCAGCAGCAGATGATGAGCGCGTGGAGAACACC] **ACTGGGACAAGCGGACTAGGGTTCAAGGGCGTGTCA**CCACC [TGACAGGCATCCATGC
CGTGGAGGAAGTCAGCCTGGAGGAGTTCT] CAGCCCATCCTGTGCCCCGAGAACATGGCG
GCTGCTCCACATCTGTATCGCAAGGGTGTGGAACACCCGCGCTGCTGTGCCCCGTG
ACCTGGTGCTCCTGCAGAACCTGCTGACTGTGGTGAGCCTCTACCTGCTCCCCGTGATC
AGTTTGATGTACCACTGGTGAGATCGACTGCATCCCCGGAGCCTGGCGCTGTGACGGCT
TCCCTGAGTGTGCTGACCAGAGTGTGAAGAAGGCTGCCCAGTGTGCTCCGCTCTCAGT
TCCCTGCGCTCGAGGCCACTGTGTGACTCGCGGTAACGCTGCGACGGTGGAGGCC
GCCAGGATCGCTCTGATGAAAGCTAACGCGATGCTGCTGTGCTGCCAACATCGATTCCGG
GCACCAAGCGGGCAGTGTGCTCATCAAGAACAGTGTGACTCCTCCCCGACTGTGCTG
ATGGGTCTGATGAGCTCATGTTGTAATCAACAAAGCCACCCCTGTGACATCCCAGCCC
ACAGCAGTGCATTGGGCCGTCAATTGGTATCATCCTCTCCCTCTGTCATGGGCCGGGG
TCTACTTTGTCGCAAGCGTGTGATGTCAGCGCTACACAGGGCCAGTGGCCCTTTC
CCCACGAGTATGTTGGTGGAGGCCCTCATGTCCTCTAACCTCATAGCCCCAGGTGGCT
CACAGCACGGTCCCTTCCCAGGCATCCCGTGCAGCAAGTCCGTGATGAGCTCCATGAGCC
TGGTGGGGGGCGCCGAGCGTGTGCCCCCTCATGACCGGAATCACGTCACGGGGCC
CCAGCAGCTCGTCCAGCACAAAGGCCACACTATATCCCGCATCTGAACCCACCCCGT
CCCCGGCCACAGACCCCTCTCTACAAACGTGGACGTGTTTATTCAGGCATCCCG
CCACCGCTAGACCATACAGGCCCTACGTCTTCAGGATATGGCACCCCCAACACACCGT
GCAGCACAGATGTGTGACAGTGTGACTACAGCATCAGTGTGCGAAGAGCAGCAAATACT
ACCTGGACTTGAAATTGGAACGGACTCACGACCCCTACCCCCCCCAGCCACCCCC
ACCTATCTGCAGAGGACAGCTGCCACCCCTACCAAGGCACTGAGAGGAGTTACTGCCACC
TCTTCCCAGCCACCGTCCCCCTGCACGGACTCGTCTGACCTCGGCCGTCAACCCGGC
CTGCTGCTCCCTGTAATTTAAATGAACAAAGGAAAATATATTATGATT
AAAAAAATAATAATTGGGTTTTAACAGTGTGAGAAATGTGAGCGGTGAAGGGTGG
GCAGGGCTGGAAACTTTCTAG

**Gene Sequence
Structure ***

3659 bp

Sequence Deleted

3701 bp

**Size of full-length
cDNA: 5119 bp**

FIGURE 3B

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Targeting Vector* (genomic sequence)

Construct Number: 992

Arm Length:

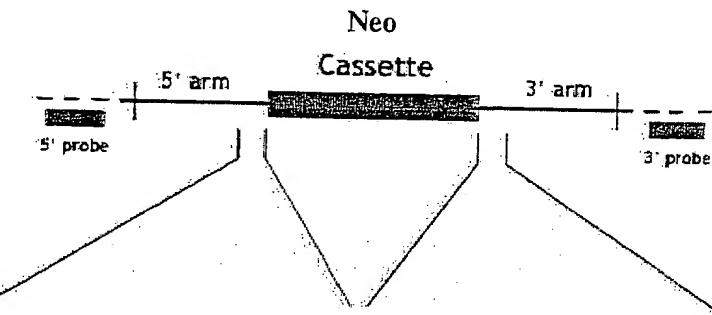
5': 1.5 kb

3': 2.9 kb

— Targeting Vector

- - - Endogenous Locus

* Not drawn to scale



5' >AAATATGCATTATCCTGAGCA
CAGTGGGTCTGGCCCTTCACTTGG
CTGCCACTCATGGAGCCTTTATGC
TAACCACAGGGGCAACCGCCCTGA
CCCTGGAAGATGCCAACATCGTAC
AGCCAGTAGGTCTGACAGTGCTGG
GCAGGCACCTCTACTGGATCGACC
GCCAGCAGCAGATGATCGAGCGTG
TGGAGAAGACC<3'
(SEQ ID NO: 7)
#3

5' >TCACTGGCATCCATGCAGTG:
AGGAAGTCAGCCTGGAGGAGTTCT
GTACGTGAGAGGGGACAGTGTGTTG
TGGTGGGGTCTCCTGGGGGAAGGT
GAATCAGCCCTACTGGCATCAGAT
GGGCTGCTGGTGCAGAGCAGTGT
GCCCTGAGGAGCTCATGGGCTCAGC
ACCGAAGGCCAGTGCATGTCCAGA
TGTCTGCCTCT<3'
(SEQ ID NO: 16)
#4

FIGURE 3C

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Phenotypic Data Summary - Open Field

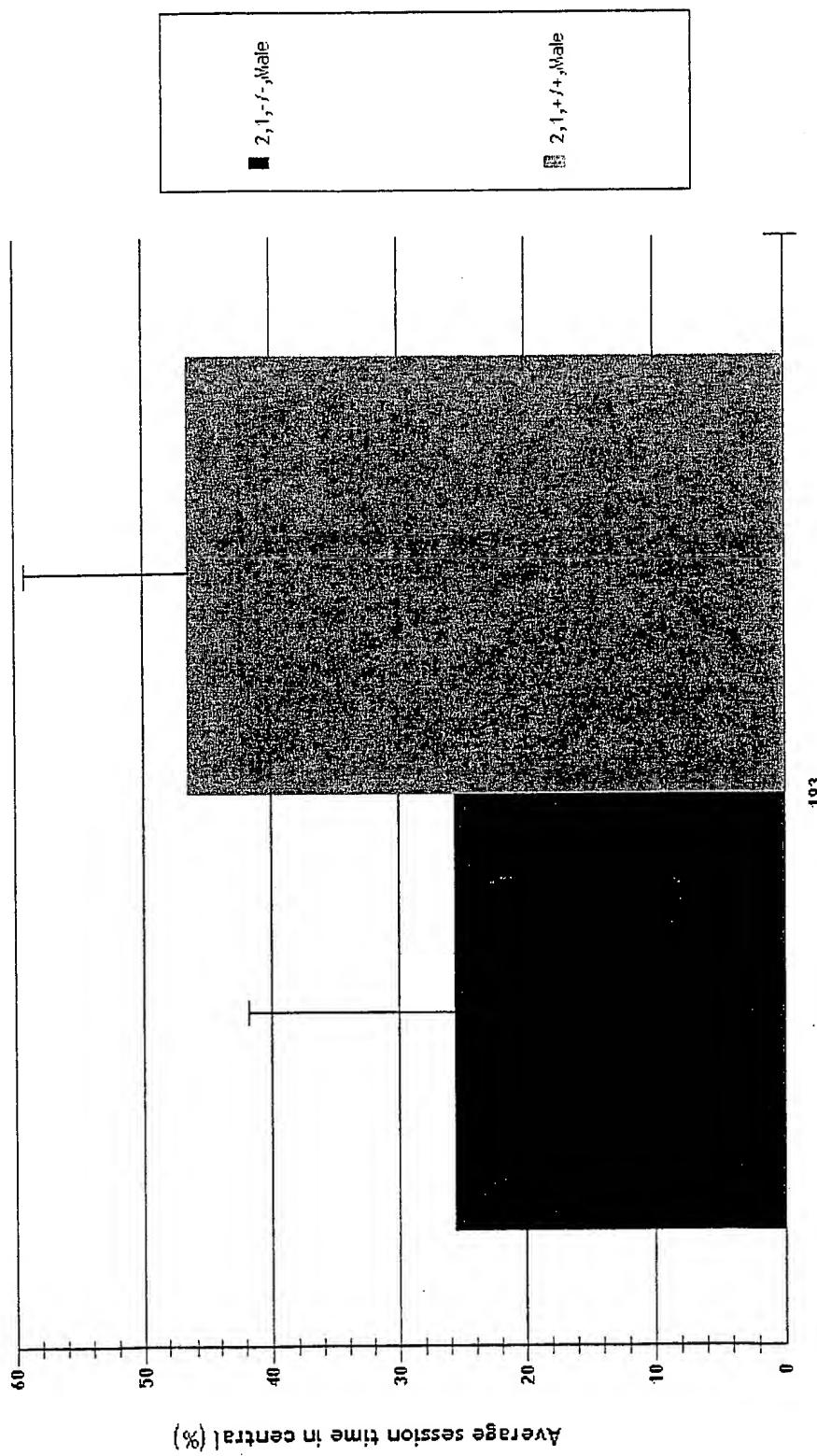


FIGURE 4

Gene

193

193 2,1,+/-,Male

Phenotypic Data Summary - Open Field

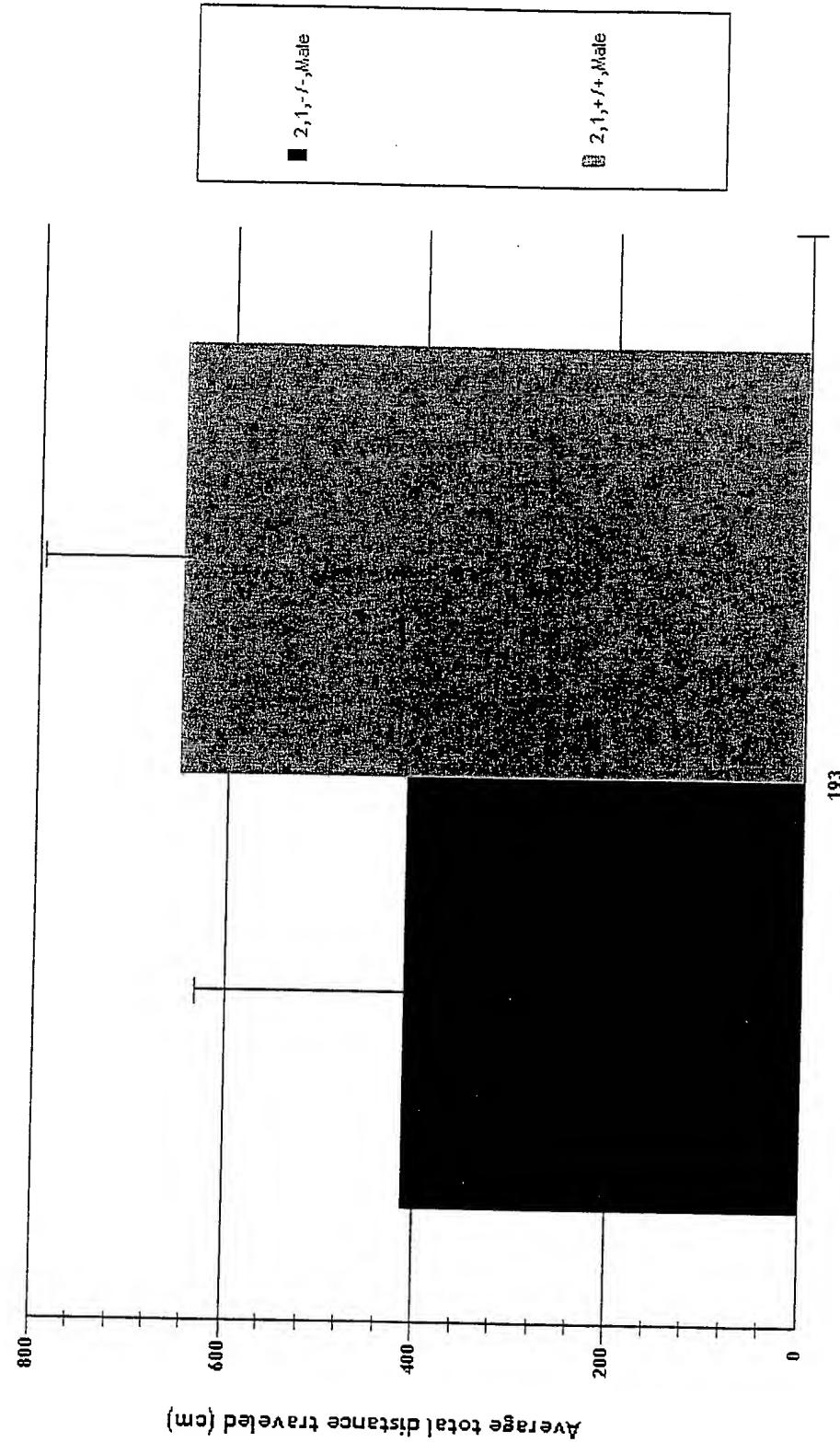


FIGURE 5